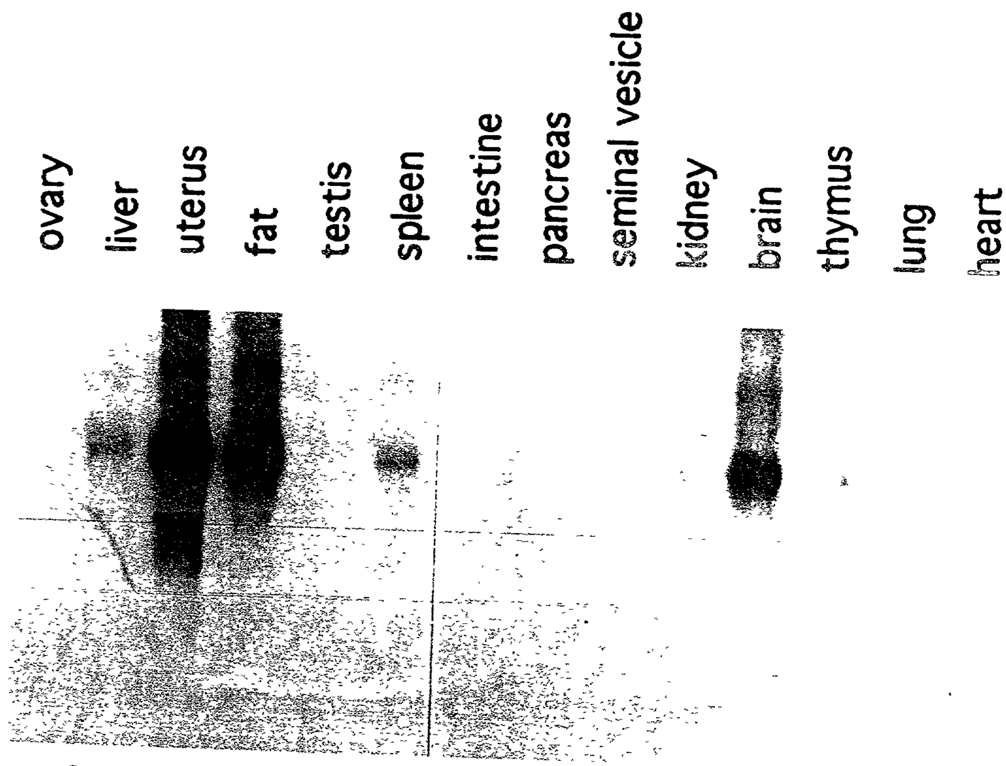

ovary
liver
uterus
fat
testis
spleen
intestine
pancreas
seminal vesicle
kidney
brain
thymus
lung
heart

FIG. 1

```
   1 TGGGGTCATCCGGGCTGTCCGAGTCCCACAGGGACAACTCCAGCCGCGGACGAGGTGCAC   60
  61 AGCCAACACTGAGCCCTCCTTGTCTGTTCTCCTGGCTCAGACCCTTCACCACCGTTACT  120
 121 CAGCCATGGCTCCAGGTCCTGCTCGGATCAGCTTGGGGTCCCAGCTGCTGCCCATGGTGC  180
        M  A  P  G  P  A  R  I  S  L  G  S  Q  L  L  P  M  V  P
 181 CGCTGCTCCTGCTGCTGCGGGGCGCAGGCTGCGGCCACAGGGGCCCCTCATGGTCCTCAT  240
      L  L  L  L  L  R  G  A  G  C  G  H  R  G  P  S  W  S  S  L
 241 TGCCCTCGGCAGCTGCCGGTCTGCAGGGGGACAGGGACTCCCAGCAGTCACCCGGGGACG  300
      P  S  A  A  A  G  L  Q  G  D  R  D  S  Q  Q  S  P  G  D  A
 301 CAGCAGCCGCTCTGGGCCCAGGCGCCCAGGACATGGTCGCTATCCACATGCTCAGGCTCT  360
      A  A  A  L  G  P  G  A  Q  D  M  V  A  I  H  M  L  R  L  Y
 361 ATGAGAAGTACAACCGAAGAGGTGCTCCACCGGGAGGAGGCAACACCGTCCGAAGCTTCC  420
      E  K  Y  N  R  R  G  A  P  P  G  G  G  N  T  V  R  S  F  R
 421 GTGCCCGGCTGGAAATGATCGACCAAAAGCCTGTGTATTTCTTCAACTTGACTTCCATGC  480
      A  R  L  E  M  I  D  Q  K  P  V  Y  F  F  N  L  T  S  M  Q
 481 AAGACTCAGAAATGATCCTCACAGCCGCCTTCCACTTCTACTCAGAACCTCCACGGTGGC  540
      D  S  E  M  I  L  T  A  A  F  H  F  Y  S  E  P  P  R  W  P
 541 CCCGGGCTGGTGAGGTATTCTGCAAGCCCCGAGCTAAGAACGCATCCTGCCGCCTCCTGA  600
      R  A  G  E  V  F  C  K  P  R  A  K  N  A  S  C  R  L  L  T
 601 CCCCAGGGCTGCCTGCACGCTTGCACCTAATCTTCCGCAGTCTTTCCCAGAACACCGCCA  660
      P  G  L  P  A  R  L  H  L  I  F  R  S  L  S  Q  N  T  A  T
 661 CTCAGGGGCTGCTCCGCGGGGCCATGGCCCTGACGCCTCCACCACGTGGCCTGTGGCAGG  720
      Q  G  L  L  R  G  A  M  A  L  T  P  P  P  R  G  L  W  Q  A
 721 CCAAGGACATCTCCTCAATCATCAAGGCTGCCCGAAGGGATGGAGAGCTGCTTCTCTCTG  780
      K  D  I  S  S  I  I  K  A  A  R  R  D  G  E  L  L  L  S  A
 781 CTCAGCTGGATACTGGGGAGAAGGACCCCGGAGTGCCACGGCCCAGTTCCCACATGCCCT  840
      Q  L  D  T  G  E  K  D  P  G  V  P  R  P  S  S  H  M  P  Y
 841 ATATCCTTGTCTACGCCAATGACCTGGCCATCTCCGAACCCAACAGTGTAGCAGTGTCGC  900
      I  L  V  Y  A  N  D  L  A  I  S  E  P  N  S  V  A  V  S  L
 901 TACAGAGATACGACCCATTTCCAGCTGGAGACTTTGAGCCTGGAGCAGCCCCCAACAGCT  960
      Q  R  Y  D  P  F  P  A  G  D  F  E  P  G  A  A  P  N  S  S
 961 CAGCTGATCCCCGCGTGCGCAGGGCGGCTCAGGTGTCAAAACCCCTGCAAGACAATGAAC 1020
      A  D  P  R  V  R  R  A  A  Q  V  S  K  P  L  Q  D  N  E  L
```

FIG. 2A

```
1021 TGCCGGGGCTGGATGAAAGACCAGCGCCTGCCCTGCATGCCCAGAATTTCCACAAGCACG 1080
       P  G  L  D  E  R  P  A  P  A  L  H  A  Q  N  F  H  K  H  E
1081 AGTTCTGGTCCAGTCCTTTCCGGGCACTGAAACCCCGCACGGCGCGCAAAGACCGCAAGA 1140
       F  W  S  S  P  F  R  A  L  K  P  R  T  A  R  K  D  R  K  K
1141 AGAAGGACCAGGACACATTCACCGCCGCCTCCTCTCAGGTGCTGGACTTTGACGAGAAGA 1200
       K  D  Q  D  T  F  T  A  A  S  S  Q  V  L  D  F  D  E  K  T
1201 CGATGCAGAAAGCCAGGAGGCGGCAGTGGGATGAGCCCCGGGTCTGCTCCAGGAGGTACC 1260
       M  Q  K  A  R  R  R  Q  W  D  E  P  R  V  C  S  R  R  Y  L
1261 TGAAGGTGGATTTTGCAGACATCGGGTGGAATGAATGGATCATCTCTCCCAAATCCTTTG 1320
       K  V  D  F  A  D  I  G  W  N  E  W  I  I  S  P  K  S  F  D
1321 ACGCCTACTACTGTGCTGGGGCCTGCGAGTTCCCCATGCCCAAGATTGTCCGCCCATCCA 1380
       A  Y  Y  C  A  G  A  C  E  F  P  M  P  K  I  V  R  P  S  N
1381 ACCATGCCACCATCCAGAGCATCGTCAGAGCTGTGGGCATTGTCCCTGGCATCCCAGAGC 1440
       H  A  T  I  Q  S  I  V  R  A  V  G  I  V  P  G  I  P  E  P
1441 CATGCTGTGTTCCAGACAAGATGAACTCCCTTGGAGTCCTTTTCCTGGATGAAAATCGGA 1500
       C  C  V  P  D  K  M  N  S  L  G  V  L  F  L  D  E  N  R  N
1501 ATGCGGTTCTGAAGGTGTACCCCAATATGTCCGTAGAGACCTGTGCCTGTCGGTAAGATG 1560
       A  V  L  K  V  Y  P  N  M  S  V  E  T  C  A  C  R  *
1561 GCTTCAAGATAGAAGACAGACCTGCTTCATCCCTGCCCTGCAGAGTGGCAATCTTGGAGC 1620
1621 CAGGGACTTGACTCGGGGAGGTTCCAGGTGCTAGACAGAGCTTACAGGCAGCCCTGCTGG 1680
1681 GACCAAGAAAGATCTGCCCACCACATCGCAATTCTTCACTTCTTCCGTGCTGGTGGTAGC 1740
1741 TCTGTAAAGACGTGTTGAGTTCCTGGAAGAAATCTGGAATTAACTGTGGTCTGCAATTTG 1800
1801 CCCATCATCCCTGCCCACACTTTTCAAGGCCTAGAAATAACGTGTGTCCTCAAATGTCAA 1860
1861 CTCCAGGCATTTGTCCTCTCAAAACCTAGAAAGACTATGCAAATCTTGGGGTACTCCCCC 1920
1921 CCCCCATGGCAGTTTAAATGCTGTTTTAAAACCCTCAGGCTGCATTCTAGAAACAGGGCC 1980
1981 TAACCCATGGCACGAGTGAGTATTTTCTCTTACGTTTCACTACACGTGCTTTTATACATG 2040
2041 CAGTATGCACATGTAATCACGGTTGATTTCTTCTTTTAATATATGTATTTCTATTTCAAA 2100
2101 GCAAAACGGAGAGAGTCGATCCCATCCCCTGCAGAGGTAATAATGCAAGTTAGGTGTGGG 2160
2161 TTGTCTAAGCATGTGTATGGAAATAATACATACAGTAATATGCTGGAATACTAAAAAAGT 2220
2221 AACCAAGATTTTATATTTTTGTAAATTATACTTTGTATACTGTAGATTGTGAGTGTTCTG 2280
2281 TGTTTTTATGGAAAGCTAATAAATTAAAGGTGCGGAGGTATC 2322
```

FIG. 2B

```
GDF-10        EKSMQKARRRQWDEPRVCSRRYLKVDF-ADIGWNEWIISPKSFDAYYCAGACEFPMPKIVRPS--

GDF-1         RPRRDAEPVLGGGPGGACRARRLYVSF-REVGWHRWVIAPRGFLANYCQGQCALPVALSGSGGPP
GDF-3         RKRRAAISVPKGFCRNFCHRHQLFINF-QDLGWHKWVIAPKGFMANYCHGECPFSMTTYLNS---
GDF-9         SFNLSEYFKQFLFPQNECELHDFRLSF-SQLKWDNWIVAPHRYNPRYCKGDCPRAVRHRYGS---
BMP-2         REKRQAKHKQRKRLKSSCKRHPLYVDF-SDVGWNDWIVAPPGYHAFYCHGECPFPLADHLNS---
BMP-4         KRSPKHHSQRARKKNKNCRRHSLYVDF-SDVGWNDWIVAPPGYQAFYCHGDCPFPLADHLNS---
Vgr-1         SRGSGSSDYNGSELKTACKKHELYVSF-QDLGWQDWIIAPKGYAANYCDGECSFPLNAHMNA---
OP-1          LRMANVAENSSSDQRQACKKHELYVSF-RDLGWQDWIIAPEGYAAYYCEGECAFPLNSYMNA---
BMP-5         SRMSSVGDYNTSEQKQACKKHELYVSF-RDLGWQDWIIAPEGYAAFYCDGECSFPLNAHMNA---
OP-2          RLPGIFDDVHGSHGRQVCRRHELYVSF-QDLGWLDWVIAPQGYSAYYCEGECSFPLDSCMNA---
BMP-3         EQTLKKARRKQWIEPRNCARRYLKVDF-ADIGWSEWIISPKSFDAYYCSGACQFPMPKSLKPS--
MIS           GPGRAQRSAGATAADGPCALRELSVDL----RAERSVLIPETYQANNCQGVCGWPQSDRNPRY--
Inhibin α     ALRLLQRPPEEPAAHANCHRVALNISF-QELGWERWIVYPPSFIFHYCHGGCGLHIPPNLSLPV-
Inhibin ßA   RRRRRGLECDGKV--NICCKKQFFVSF-KDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSL-
Inhibin ßB   RIRKRGLECDGRT--NLCCRQQFFIDF-RLIGWNDWIIAPTGYYGNYCEGSCPAYLAGVPGSAS-
Nodal         GWGRRQRRHHLPDRSQLCRRVKFQVDF-NLIGWGSWIIYPKQYNAYRCEGECPNPVGEEFHP---
TGF-ß1        RRALDTNYCFSSTE-KNCCVRQLYIDFRKDLGWK-WIHEPKGYHANFCLGPCPYIWSLD------
TGF-ß2        KRALDAAYCFRNVQ-DNCCLRPLYIDFKRDLGWK-WIHEPKGYNANFCAGACPYLWSSD------
TGF-ß3        KRALDTNYCFRNLE-ENCCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPYLRSAD------
```

FIG. 3A

GDF-10	--NHATIQSIVRA-VGIVPGIPEPCCV--PDKMNSLGVLFL-DENRNAVLKVYPNMSVETCACR
GDF-1	ALNHAVLRALMHA--AAPGAADLPCCV--PARLSPISVLFF-DNSDNVVLRQYEDMVVDECGCR
GDF-3	-SNYAFMQALMHM---ADPKVPKAVCV--PTKLSPISMLYQ-DSDKNVILRHYEDMVVDECGCG
GDF-9	-PVHTMVQNIIYE--KLDPSVPRPSCV--PGKYSPLSVLTI-EPDGSIAYKEYEDMIATRCTCR
BMP-2	-TNHAIVQTLVNS---VNSKIPKACCV--PTELSAISMLYL-DENEKVVLKNYQDMVVEGCGCR
BMP-4	-TNHAIVQTLVNS---VNSSIPKACCV--PTELSAISMLYL-DEYDKVVLKNYQEMVVEGCGCR
Vgr-1	-TNHAIVQTLVHL--MNPEYVPKPCCA--PTKLNAISVLYF-DDNSNVILKKYRNMVVRACGCH
OP-1	-TNHAIVQTLVHF--INPETVPKPCCA--PTQLNAISVLYF-DDSSNVILKKYRNMVVRACGCH
BMP-5	-TNHAIVQTLVHL--MFPDHVPKPCCA--PTKLNAISVLYF-DDSSNVILKKYRNMVVRSCGCH
OP-2	-TNHAILQSLVHL--MKPNAVPKACCA--PTKLSATSVLYY-DSSNNVILRKARNMVVKACGCH
BMP-3	--NHATIQSIVRA-VGVVPGIPEPCCV--PEKMSSLSILFF-DENKNVVLKVYPNMTVESCACR
MIS	-GNHVVLLLKMQA--RGAALARPPCCV--PTAYAGKLLISLSEER--ISAHHVPNMVATECGCR
Inhibin α	-PGAPPTPAQPYS----LLPGAQPCCAALPGTMRPLHVRTTSDGGYSFKYETVPNLLTQHCACI
Inhibin ßA	-SFHSTVINHYRMRGHSPFANLKSCCV--PTKLRPMSMLYY-DDGQNIIKKDIQNMIVEECGCS
Inhibin ßB	-SFHTAVVNQYRMRGLNPGT-VNSCCI--PTKLSTMSMLYF-DDEYNIVKRDVPNMIVEECGCA
Nodal	-TNHAYIQSLLKR--YQPHRVPSTCCA--PVKTKPLSMLYV--DNGRVLLEHHKDMIVEECGCL
TGF-ß1	-TQYSKVLALYNQ--HNPGASAAPCCV--PQALEPLPIVYY-VGRKPKV-EQLSNMIVRSCKCS
TGF-ß2	-TQHSRVLSLYNT--INPEASASPCCV--SQDLEPLTILYY-IGKTPKI-EQLSNMIVKSCKCS
TGF-ß3	-TTHSTVLGLYNT--LNPEASASPCCV--PQDLEPLTILYY-VGRTPKV-EQLSNMVVKSCKCS

FIG. 3B

	% amino acid identity with GDF-10
GDF-1	38%
GDF-3	37%
GDF-9	28%
BMP-2	46%
BMP-4	45%
Vgr-1	43%
OP-1	41%
BMP-5	41%
OP-2	39%
BMP-3	83%
MIS	31%
Inhibin α	28%
Inhibin βA	36%
Inhibin βB	35%
Nodal	40%
TGF-β1	30%
TGF-β2	30%
TGF-β3	29%

FIG. 4

```
         .         .         .         .         .
KARRKQWDEPRVCSRRYLKVDFADIGWNEWIISPKSFDAYYCAGACEFPM
||||:|||||||||||||||||||||||||||||||||||||||||||||
KARRRQWDEPRVCSRRYLKVDFADIGWNEWIISPKSFDAYYCAGACEFPM

         .         .         .         .         .
PKIVRPSNHATIQSIVRAVGIIPGIPEPCCVPDKMNSLGVLFLDENRNVV
|||||||||||||||||||||:||||||||||||||||||||||||||.|
PKIVRPSNHATIQSIVRAVGIVPGIPEPCCVPDKMNSLGVLFLDENRNAV

         .
LKVYPNMSVDTCACR
|||||||||:|||||
LKVYPNMSVETCACR
```

FIG. 5

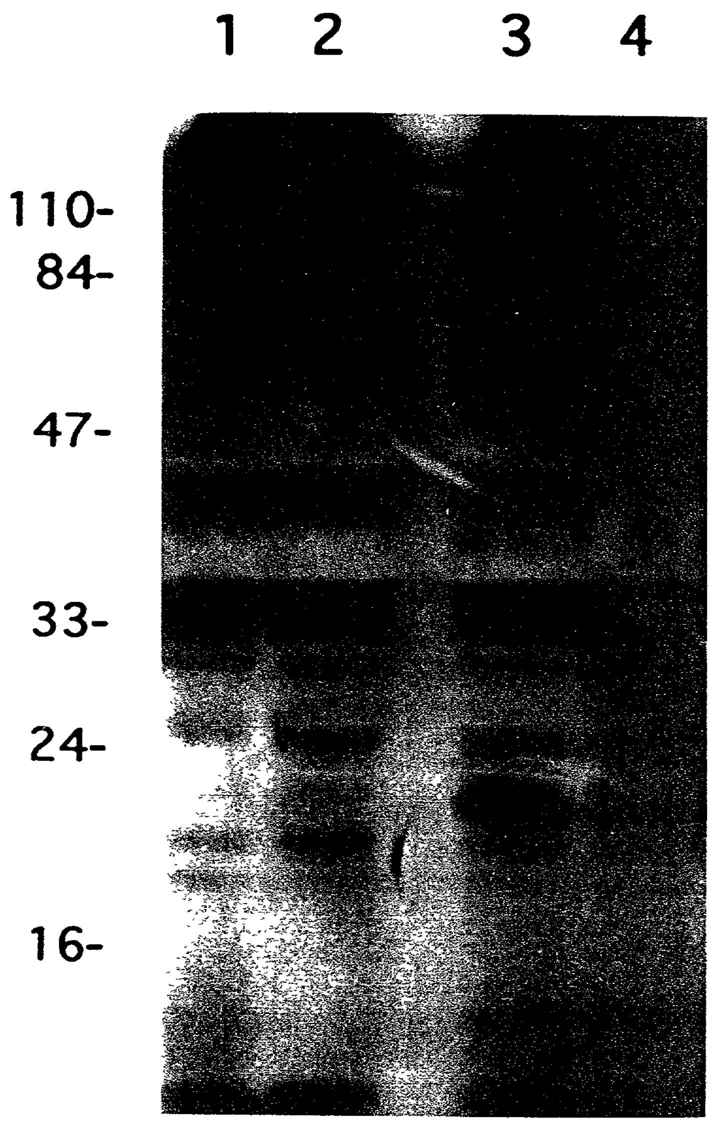

FIG. 6